

REPLACEMENT SHEET

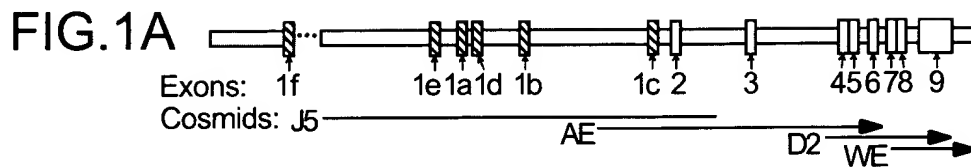
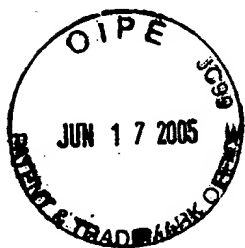
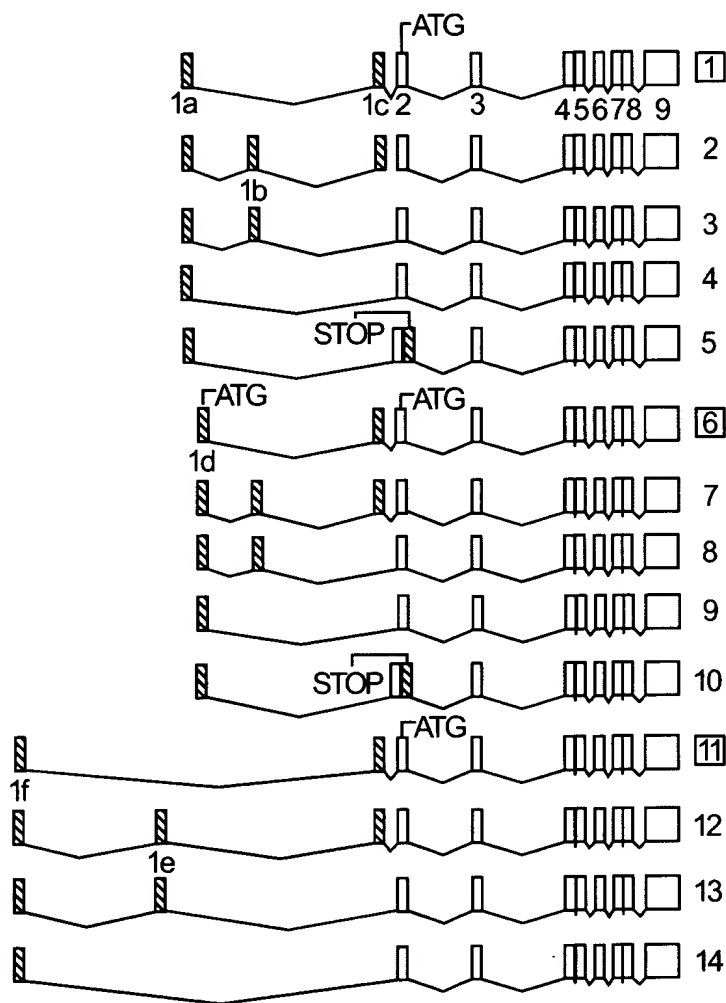


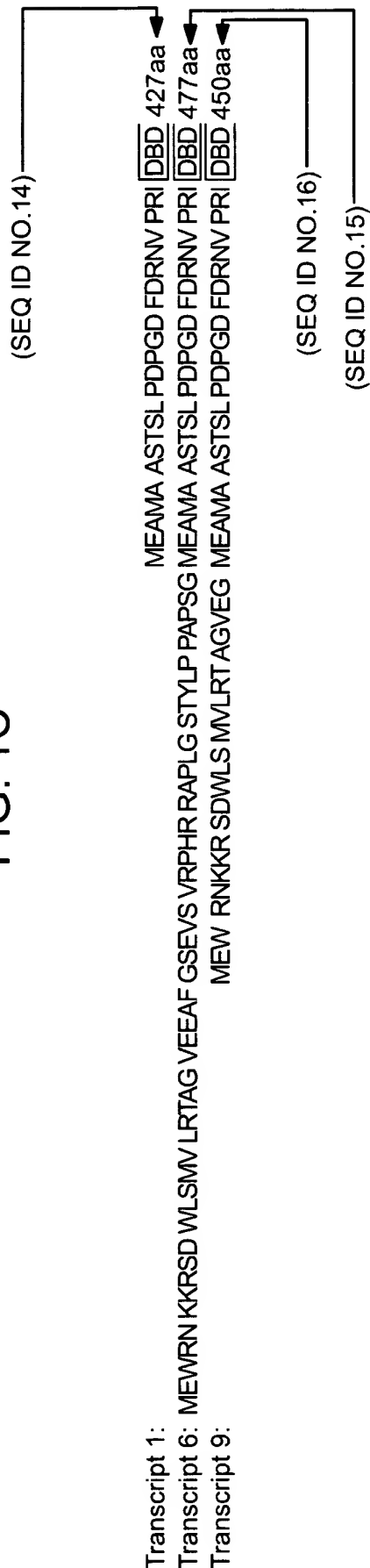
FIG.1B





REPLACEMENT SHEET

FIG. 1C



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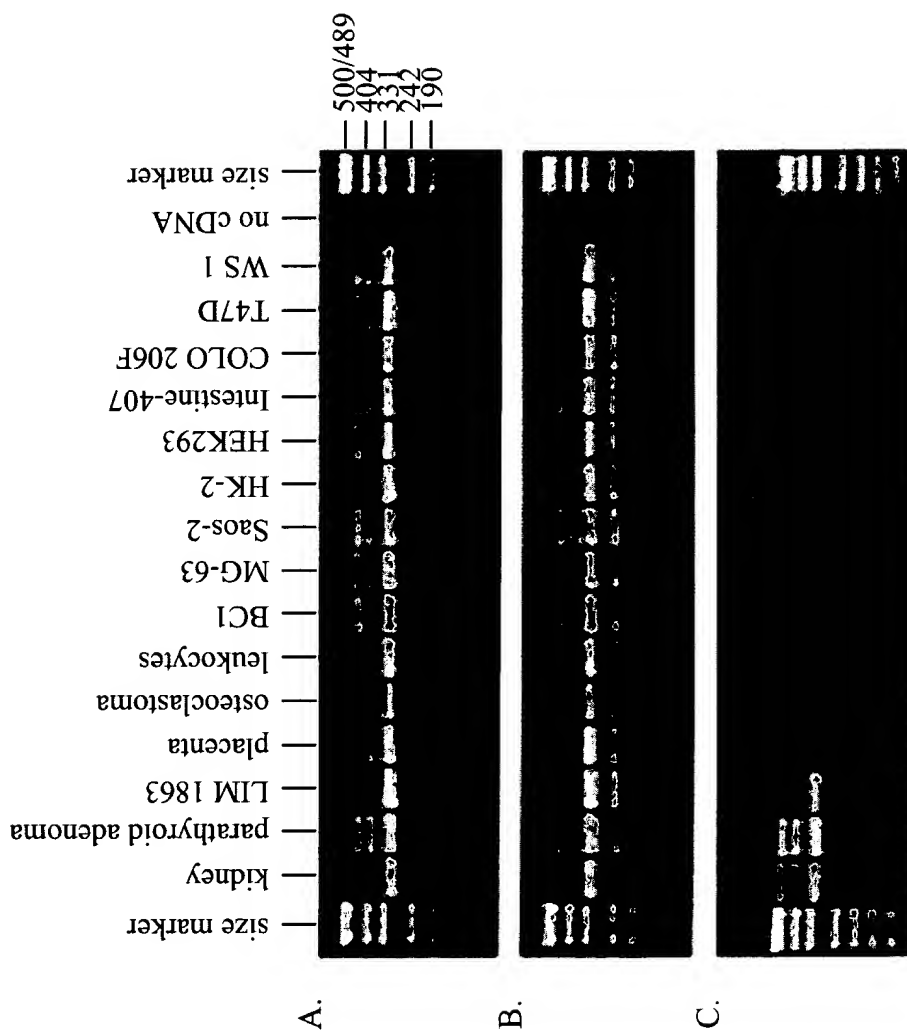
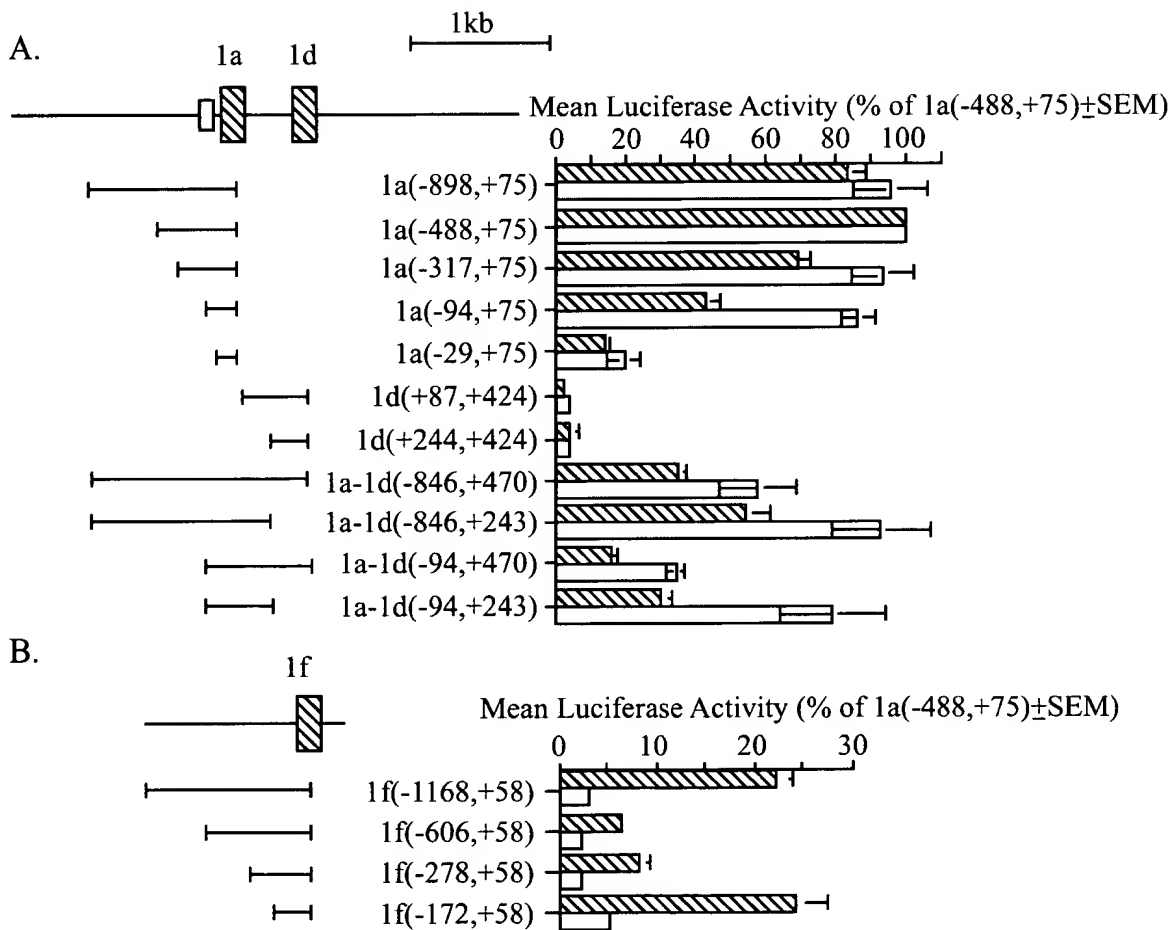


FIG. 2

REPLACEMENT SHEET



FIG. 3



REPLACEMENT SHEET



FIG. 4

- A. 5'...atcccttaag GGCTCCTGAACCTAGCCCAGCTGGACGGAG
AAATGGACTCTAGCCTCCTCTGATAGCCTCATGCCAGGCC
CGTGACATTGCTTTGCTTGCCCTCAATCCTCATAGCT
TCTCTTTGGGgtaagtacag...3' (SEQ ID NO: 13)
- B. 5'...TGCGACCTTGGCGGTGAGCCTGGGGACAGGGGTGAGGC
CAGAGACGGAACGACGAGGGGCGCCGAGGCGAGGG
AGAACAGCGGCACTAAGGCAGAAAGGAAGAGGGCGGTGTG
TTCACCCGCAGCCCAATCCATCACTCAGCAACTCCTAGAC
GCTGGTAGAAAGTTCTCCGAGGAGCCTGCCATCCAGTCGT
GCGTGCAG...3' (SEQ ID NO: 5)
- C. 5'...tgtttttag AGGCAGCATGAAACAGTGGGATGTGCAGAG
AGAAGATCTGGGTCCAGTAGCTCTGACACTCCTCAGCTGT
AGAAACCTTGACAACTCTGCACATCAGTTGTACAATGGAA
CGGTATTTTTTACTCTTCATGTCTGAAAAGGCTATGATAA
AGATCAAgtaagatatt...3' (SEQ ID NO: 6)
- D. 5'...GTTTCCTTCTTCTGTGCGGGGCGCCTTGGC[ATG]GAGTGG
AGGAATAAGAAAAGGAGCGATTGGCTGTGATG[GTG]CTCA
GAACTGCTGGAGTGGAGGgtgtgtaacc...3' (SEQ ID NO: 22)

REPLACEMENT SHEET



FIG. 5A

Transcript 6

(Sequence Range: 1 to 1463)

```

      10      20      30      40      50
      *      *      *      *      *
GTTTCCTTCT TCTGTCGGGG CGCCTTGGCA TGGAGTGGAG GAATAAGAAA
CAAAGGAAGA AGACAGCCCC GCGGAACCGT ACCTCACCTC CTTATTCTTT
                                   MetGluTrpArg AsnLysLys>

      60      70      80      90     100
      *      *      *      *      *
AGGAGCGATT GGCTGTCGAT GGTGCTCAGA ACTGCTGGAG TGGAGGAAGC
TCCTCGCTAA CCGACAGCTA CCACGAGTCT TGACGACCTC ACCTCCTTCG
ArgSerAsp TrpLeuSerMet ValLeuArg ThrAlaGly ValGluGluAla>

     110     120     130     140     150
      *      *      *      *      *
CTTTGGGTCT GAAGTGTCTG TGAGACCTCA CAGAAGAGCA CCCCTGGGCT
GAAACCCAGA CTTACAGAC ACTCTGGAGT GTCTTCTCGT GGGGACCCGA
PheGlySer GluValSer ValArgProHis ArgArgAla ProLeuGly>

     160     170     180     190     200
      *      *      *      *      *
CCACTTACCT GCCCCCTGCT CCTTCAGGGA TGGAGGCAAT GGCGGCCAGC
GGTGAATGGA CGGGGGACGA GGAAGTCCCT ACCTCCGTTA CCGCCGGTCG
SerThrTyrLeu ProProAla ProSerGly MetGluAlaMet AlaAlaSer>

     210     220     230     240     250
      *      *      *      *      *
ACTTCCCTGC CTGACCCTGG AGACTTTGAC CGGAACGTGC CCCGGATCTG
TGAAGGGACG GACTGGGACC TCTGAAACTG GCCTTGACAG GGGCCTAGAC
ThrSerLeu ProAspProGly AspPheAsp ArgAsnVal ProArgIleCys>

     260     270     280     290     300
      *      *      *      *      *
TGGGGTGTGT GGAGACCGAG CCACTGGCTT TCACTTCAAT GCTATGACCT
ACCCACACA CCTCTGGCTC GGTGACCGAA AGTGAAGTTA CGATACTGGA
GlyValCys GlyAspArg AlaThrGlyPhe HisPheAsn AlaMetThr>

     310     320     330     340     350
      *      *      *      *      *
GTGAAGGCTG CAAAGGCTTC TTCAGGCGAA GCATGAAGCG GAAGGCACTA
CACTTCCGAC GTTTCGGAAG AAGTCCGCTT CGTACTTCGC CTTCCGTGAT
CysGluGlyCys LysGlyPhe PheArgArg SerMetLysArg LysAlaLeu>

     360     370     380     390     400
      *      *      *      *      *
TTCACCTGCC CCTTCAACGG GGAAGTCCGC ATCACCAAGG ACAACCGACG
AAGTGGACGG GGAAGTTGCC CCTGACGGCG TAGTGGTTCC TGTGGCTGCG
PheThrCys ProPheAsnGly AspCysArg IleThrLys AspAsnArgArg>
```

REPLACEMENT SHEET

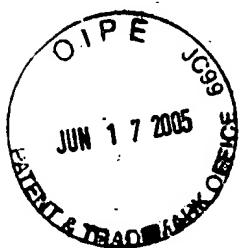


FIG. 5B

```

      410      420      430      440      450
      *      *      *      *      *
CCACTGCCAG GCCTGCCGGC TCAAACGCTG TGTGGACATC GGCATGATGA
GGTGACGGTC CGGACGGCCG AGTTTGCAC ACACCTGTAG CCGTACTACT
HisCysGln AlaCysArg LeuLysArgCys ValAspIle GlyMetMet>

      460      470      480      490      500
      *      *      *      *      *
AGGAGTTCAT TCTGACAGAT GAGGAAGTGC AGAGGAAGCG GGAGATGATC
TCCTCAAGTA AGACTGTCTA CTCCTTCACG TCTCCTTCGC CCTCTACTAG
LysGluPheIle LeuThrAsp GluGluVal GlnArgLysArg GluMetIle>

      510      520      530      540      550
      *      *      *      *      *
CTGAAGCGGA AGGAGGAGGA GGCCTTGAAG GACAGTCTGC GGCCCAAGCT
GACTTCGCCT TCCTCCTCCT CCGGAAC TTCGTCAGACG CCGGGTTCGA
LeuLysArg LysGluGluGlu AlaLeuLys AspSerLeu ArgProLysLeu>

      560      570      580      590      600
      *      *      *      *      *
GTCTGAGGAG CAGCAGCGCA TCATTGCCAT ACTGCTGGAC GCCCACCATA
CAGACTCCTC GTCGTCGCGT AGTAACGGTA TGACGACCTG CCGGTGGTAT
SerGluGlu GlnGlnArg IleIleAlaIle LeuLeuAsp AlaHisHis>

      610      620      630      640      650
      *      *      *      *      *
AGACCTACGA CCCCACCTAC TCCGACTTCT GCCAGTCCG GCCTCCAGTT
TCTGGATGCT GGGGTGGATG AGGCTGAAGA CGGTCAAGGC CGGAGGTCAA
LysThrTyrAsp ProThrTyr SerAspPhe CysGlnPheArg ProProVal>

      660      670      680      690      700
      *      *      *      *      *
CGTGTGAATG ATGGTGGAGG GAGCCATCCT TCCAGGCCCA ACTCCAGACA
GCACACTTAC TACCACCTCC CTCGGTAGGA AGGTCCGGGT TGAGGTCTGT
ArgValAsn AspGlyGlyGly SerHisPro SerArgPro AsnSerArgHis>

      710      720      730      740      750
      *      *      *      *      *
CACTCCCAGC TTCTCTGGGG ACTCCTCCTC CTCCTGCTCA GATCACTGTA
GTGAGGGTCG AAGAGACCCC TGAGGAGGAG GAGGACGAGT CTAGTGACAT
ThrProSer PheSerGly AspSerSerSer SerCysSer AspHisCys>

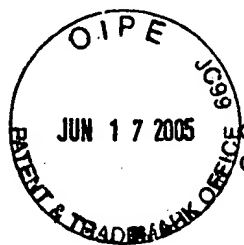
      760      770      780      790      800
      *      *      *      *      *
TCACCTCTTC AGACATGATG GACTCGTCCA GCTTCTCCAA TCTGGATCTG
AGTGGAGAAG TCTGTACTAC CTGAGCAGGT CGAAGAGGTT AGACCTAGAC
IleThrSerSer AspMetMet AspSerSer SerPheSerAsn LeuAspLeu>

      810      820      830      840      850
      *      *      *      *      *
AGTGAAGAAG ATTCAGATGA CCCTTCTGTG ACCCTAGAGC TGTCCCAGCT
TCACTTCTTC TAAGTCTACT GGGAAGACAC TGGGATCTCG ACAGGGTCGA
SerGluGlu AspSerAspAsp ProSerVal ThrLeuGlu LeuSerGlnLeu>

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REPLACEMENT SHEET

FIG. 5C



```
      860      870      880      890      900
      *      *      *      *      *
CTCCATGCTG CCCCACCTGG CTGACCTGGT CAGTTACAGC ATCCAAAAGG
GAGGTACGAC GGGGTGGACC GACTGGACCA GTCAATGTCG TAGGTTTTCC
SerMetLeu ProHisLeu AlaAspLeuVal SerTyrSer IleGlnLys>

      910      920      930      940      950
      *      *      *      *      *
TCATTGGCTT TGCTAAGATG ATACCAGGAT TCAGAGACCT CACCTCTGAG
AGTAACCGAA ACGATTCTAC TATGGTCCTA AGTCTCTGGA GTGGAGACTC
ValIleGlyPhe AlaLysMet IleProGly PheArgAspLeu ThrSerGlu>

      960      970      980      990     1000
      *      *      *      *      *
GACCAGATCG TACTGCTGAA GTCAAGTGCC ATTGAGGTCA TCATGTTGCG
CTGGTCTAGC ATGACGACTT CAGTTCACGG TAACTCCAGT AGTACAACGC
AspGlnIle ValLeuLeuLys SerSerAla IleGluVal IleMetLeuArg>

     1010     1020     1030     1040     1050
      *      *      *      *      *
CTCCAATGAG TCCTTCACCA TGGACGACAT GTCCTGGACC TGTGGCAACC
GAGGTTACTC AGGAAGTGGT ACCTGCTGTA CAGGACCTGG ACACCGTTGG
SerAsnGlu SerPheThr MetAspAspMet SerTrpThr CysGlyAsn>

     1060     1070     1080     1090     1100
      *      *      *      *      *
AAGACTACAA GTACCGCGTC AGTGACGTGA CCAAAGCCGG ACACAGCCTG
TTCTGATGTT CATGGCGCAG TCACTGCACT GGTTCGCGCC TGTGTGCGAC
GlnAspTyrLys TyrArgVal SerAspVal ThrLysAlaGly HisSerLeu>

     1110     1120     1130     1140     1150
      *      *      *      *      *
GAGCTGATTG AGCCCCTCAT CAAGTTCCAG GTGGGACTGA AGAAGCTGAA
CTCGACTAAC TCGGGGAGTA GTTCAAGGTC CACCTGACT TCTTCGACTT
GluLeuIle GluProLeuIle LysPheGln ValGlyLeu LysLysLeuAsn>

     1160     1170     1180     1190     1200
      *      *      *      *      *
CTTGCATGAG GAGGAGCATG TCCTGCTCAT GGCCATCTGC ATCGTCTCCC
GAACGTACTC CTCCTCGTAC AGGACGAGTA CCGGTAGACG TAGCAGAGGG
LeuHisGlu GluGluHis ValLeuLeuMet AlaIleCys IleValSer>

     1210     1220     1230     1240     1250
      *      *      *      *      *
CAGATCGTCC TGGGGTGCAG GACGCCGCGC TGATTGAGGC CATCCAGGAC
GTCTAGCAGG ACCCCACGTC CTGCGGCGCG ACTAACTCCG GTAGGTCCTG
ProAspArgPro GlyValGln AspAlaAla LeuIleGluAla IleGlnAsp>

     1260     1270     1280     1290     1300
      *      *      *      *      *
CGCCTGTCCA ACACACTGCA GACGTACATC CGCTGCCGCC ACCCGCCCCC
GCGGACAGGT TGTGTGACGT CTGCATGTAG GCGACGGCGG TGGGCGGGGG
ArgLeuSer AsnThrLeuGln ThrTyrIle ArgCysArg HisProProPro>
```


Title: "ISOFORMS OF THE HUMAN VITAMIN D
RECEPTOR"

Inventor: LINDA ANNE CROFTS, ET AL.

Application No.: 09/509,482

Atty. Docket No.: RICE-014

REPLACEMENT SHEET

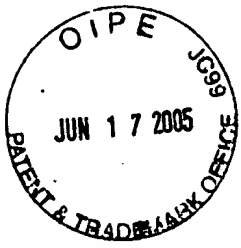


FIG. 5D

```

      1310      1320      1330      1340      1350
      *      *      *      *      *      *      *
GGGCAGCCAC CTGCTCTATG CCAAGATGAT CCAGAAGCTA GCCGACCTGC
CCCGTCGGTG GACGAGATAC GGTCTCTACTA GGTCTTCGAT CGGCTGGACG
GlySerHis LeuLeuTyr AlaLysMetIle GlnLysLeu AlaAspLeu>

      1360      1370      1380      1390      1400
      *      *      *      *      *      *      *
GCAGCCTCAA TGAGGAGCAC TCCAAGCAGT ACCGCTGCCT CTCCTTCCAG
CGTCGGAGTT ACTCCTCGTG AGGTTCGTCA TGGCGACGGA GAGGAAGGTC
ArgSerLeuAsn GluGluHis SerLysGln TyrArgCysLeu SerPheGln>

      1410      1420      1430      1440      1450
      *      *      *      *      *      *      *
CCTGAGTGCA GCATGAAGCT AACGCCCCCTT GTGCTCGAAG TGTTTGGCAA
GGACTCACGT CGTACTTCGA TTGCGGGGAA CACGAGCTTC ACAAACCGTT
ProGluCys SerMetLysLeu ThrProLeu ValLeuGlu ValPheGlyAsn>

      1460
      *      *
TGAGATCTCC TGA (SEQ ID NO:2)
ACTCTAGAGG ACT (SEQ ID NO:17)
GluIleSer ***> (SEQ ID NO:9)
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REPLACEMENT SHEET



FIG. 6A

Transcript 9

(Sequence range: 1 to 1382)

```

      10      20      30      40      50
      *      *      *      *      *
GTTTCCTTCT TCTGTCGGGG CGCCTTGGA TGGAGTGGAG GAATAAGAAA
CAAAGGAAGA AGACAGCCCC GCGGAACCGT ACCTCACCTC CTTATTCTTT
                               MetGluTrpArg AsnLysLys>

      60      70      80      90     100
      *      *      *      *      *
AGGAGCGATT GGCTGTCGAT GGTGCTCAGA ACTGCTGGAG TGGAGGGGAT
TCCTCGCTAA CCGACAGCTA CCACGAGTCT TGACGACCTC ACCTCCCCTA
ArgSerAsp TrpLeuSerMet ValLeuArg ThrAlaGly ValGluGlyMet>

     110     120     130     140     150
      *      *      *      *      *
GGAGGCAATG GCGGCCAGCA CTTCCCTGCC TGACCCTGGA GACTTTGACC
CCTCCGTTAC CGCCGGTCGT GAAGGGACGG ACTGGGACCT CTGAAACTGG
GluAlaMet AlaAlaSer ThrSerLeuPro AspProGly AspPheAsp>

     160     170     180     190     200
      *      *      *      *      *
GGAACGTGCC CCGGATCTGT GGGGTGTGTG GAGACCGAGC CACTGGCTTT
CCTTGCACGG GGCCTAGACA CCCCACACAC CTCTGGCTCG GTGACCGAAA
ArgAsnValPro ArgIleCys GlyValCys GlyAspArgAla ThrGlyPhe>

     210     220     230     240     250
      *      *      *      *      *
CACTTCAATG CTATGACCTG TGAAGGCTGC AAAGGCTTCT TCAGGCGAAG
GTGAAGTTAC GATACTGGAC ACTTCCGACG TTTCCGAAGA AGTCCGCTTC
HisPheAsn AlaMetThrCys GluGlyCys LysGlyPhe PheArgArgSer>

     260     270     280     290     300
      *      *      *      *      *
CATGAAGCGG AAGGCACTAT TCACCTGCCC CTTCAACGGG GACTGCCGCA
GTACTTCGCC TTCCGTGATA AGTGGACGGG GAAGTTGCCC CTGACGGCGT
MetLysArg LysAlaLeu PheThrCysPro PheAsnGly AspCysArg>

     310     320     330     340     350
      *      *      *      *      *
TCACCAAGGA CAACCGACGC CACTGCCAGG CCTGCCGGCT CAAACGCTGT
AGTGGTTTCT GTTGGCTGCG GTGACGGTCC GGACGGCCGA GTTTGCGACA
IleThrLysAsp AsnArgArg HisCysGln AlaCysArgLeu LysArgCys>

     360     370     380     390     400
      *      *      *      *      *
GTGGACATCG GCATGATGAA GGAGTTCATT CTGACAGATG AGGAAGTGCA
CACCTGTAGC CGTACTACTT CCTCAAGTAA GACTGTCTAC TCCTTCACGT
ValAspIle GlyMetMetLys GluPheIle LeuThrAsp GluGluValGln>
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REPLACEMENT SHEET



FIG. 6B

```

      410      420      430      440      450
      *      *      *      *      *
GAGGAAGCGG GAGATGATCC TGAAGCGGAA GGAGGAGGAG GCCTTGAAGG
CTCCTTCGCC CTCTACTAGG ACTTCGCCTT CCTCCTCCTC CGGAACCTCC
ArgLysArg GluMetIle LeuLysArgLys GluGluGlu AlaLeuLys>

      460      470      480      490      500
      *      *      *      *      *
ACAGTCTGCG GCCCAAGCTG TCTGAGGAGC AGCAGCGCAT CATTGCCATA
TGTCAGACGC CGGGTTCGAC AGACTCCTCG TCGTCGCGTA GTAACGGTAT
AspSerLeuArg ProLysLeu SerGluGlu GlnGlnArgIle IleAlaIle>

      510      520      530      540      550
      *      *      *      *      *
CTGCTGGACG CCCACCATAA GACCTACGAC CCCACCTACT CCGACTTCTG
GACGACCTGC GGGTGGTATT CTGGATGCTG GGGTGGATGA GGCTGAAGAC
LeuLeuAsp AlaHisHisLys ThrTyrAsp ProThrTyr SerAspPheCys>

      560      570      580      590      600
      *      *      *      *      *
CCAGTTCCGG CCTCCAGTTC GTGTGAATGA TGGTGGAGGG AGCCATCCTT
GGTCAAGGCC GGAGGTCAAG CACACTTACT ACCACCTCCC TCGGTAGGAA
GlnPheArg ProProVal ArgValAsnAsp GlyGlyGly SerHisPro>

      610      620      630      640      650
      *      *      *      *      *
CCAGGCCCAA CTCCAGACAC ACTCCCAGCT TCTCTGGGGA CTCCTCCTCC
GGTCCGGGTT GAGGTCTGTG TGAGGGTCTGA AGAGACCCCT GAGGAGGAGG
SerArgProAsn SerArgHis ThrProSer PheSerGlyAsp SerSerSer>

      660      670      680      690      700
      *      *      *      *      *
TCCTGCTCAG ATCACTGTAT CACCTCTTCA GACATGATGG ACTCGTCCAG
AGGACGAGTC TAGTGACATA GTGGAGAAGT CTGTACTACC TGAGCAGGTC
SerCysSer AspHisCysIle ThrSerSer AspMetMet AspSerSerSer>

      710      720      730      740      750
      *      *      *      *      *
CTTCTCCAAT CTGGATCTGA GTGAAGAAGA TTCAGATGAC CCTTCTGTGA
GAAGAGGTTA GACCTAGACT CACTTCTTCT AAGTCTACTG GGAAGACACT
PheSerAsn LeuAspLeu SerGluGluAsp SerAspAsp ProSerVal>

      760      770      780      790      800
      *      *      *      *      *
CCCTAGAGCT GTCCCAGCTC TCCATGCTGC CCCACCTGGC TGACCTGGTC
GGGATCTCGA CAGGGTCGAG AGGTACGACG GGGTGGACCG ACTGGACCAG
ThrLeuGluLeu SerGlnLeu SerMetLeu ProHisLeuAla AspLeuVal>

      810      820      830      840      850
      *      *      *      *      *
AGTTACAGCA TCCAAAAGGT CATTGGCTTT GCTAAGATGA TACCAGGATT
TCAATGTCTG AGGTTTTCCA GTAACCGAAA CGATTCTACT ATGGTCCTAA
SerTyrSer IleGlnLysVal IleGlyPhe AlaLysMet IleProGlyPhe>

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REPLACEMENT SHEET



FIG. 6C

860	870	880	890	900
* * *	* * *	* * *	* * *	* * *
CAGAGACCTC	ACCTCTGAGG	ACCAGATCGT	ACTGCTGAAG	TCAAGTGCCA
GTCTCTGGAG	TGGAGACTCC	TGGTCTAGCA	TGACGACTTC	AGTTCACGGT
ArgAspLeu	ThrSerGlu	AspGlnIleVal	LeuLeuLys	SerSerAla>
910	920	930	940	950
* * *	* * *	* * *	* * *	* * *
TTGAGGTCAT	CATGTTGCGC	TCCAATGAGT	CCTTCACCAT	GGACGACATG
AACTCCAGTA	GTACAACGCG	AGGTTACTCA	GGAAGTGGTA	CCTGCTGTAC
IleGluValIle	MetLeuArg	SerAsnGlu	SerPheThrMet	AspAspMet>
960	970	980	990	1000
* * *	* * *	* * *	* * *	* * *
TCCTGGACCT	GTGGCAACCA	AGACTACAAG	TACCGCGTCA	GTGACGTGAC
AGGACCTGGA	CACCGTTGGT	TCTGATGTTC	ATGGCGCAGT	CACTGCACTG
SerTrpThr	CysGlyAsnGln	AspTyrLys	TyrArgVal	SerAspValThr>
1010	1020	1030	1040	1050
* * *	* * *	* * *	* * *	* * *
CAAAGCCGGA	CACAGCCTGG	AGCTGATTGA	GCCCCTCATC	AAGTTCCAGG
GTTCGGCCCT	GTGTCGGACC	TCGACTAACT	CGGGGAGTAG	TTCAAGGTCC
LysAlaGly	HisSerLeu	GluLeuIleGlu	ProLeuIle	LysPheGln>
1060	1070	1080	1090	1100
* * *	* * *	* * *	* * *	* * *
TGGGACTGAA	GAAGCTGAAC	TTGCATGAGG	AGGAGCATGT	CCTGCTCATG
ACCCTGACTT	CTTCGACTTG	AACGTACTCC	TCCTCGTACA	GGACGAGTAC
ValGlyLeuLys	LysLeuAsn	LeuHisGlu	GluGluHisVal	LeuLeuMet>
1110	1120	1130	1140	1150
* * *	* * *	* * *	* * *	* * *
GCCATCTGCA	TCGTCTCCCC	AGATCGTCCT	GGGGTGCAGG	ACGCCGCGCT
CGGTAGACGT	AGCAGAGGGG	TCTAGCAGGA	CCCCACGTCC	TGCGGCGCGA
AlaIleCys	IleValSerPro	AspArgPro	GlyValGln	AspAlaAlaLeu>
1160	1170	1180	1190	1200
* * *	* * *	* * *	* * *	* * *
GATTGAGGCC	ATCCAGGACC	GCCTGTCCAA	CACACTGCAG	ACGTACATCC
CTAACTCCGG	TAGGTCCTGG	CGGACAGGTT	GTGTGACGTC	TGCATGTAGG
IleGluAla	IleGlnAsp	ArgLeuSerAsn	ThrLeuGln	ThrTyrIle>
1210	1220	1230	1240	1250
* * *	* * *	* * *	* * *	* * *
GCTGCCGCCA	CCCCCCCCCG	GGCAGCCACC	TGCTCTATGC	CAAGATGATC
CGACGGCGGT	GGGCGGGGGC	CCGTCGGTGG	ACGAGATACG	GTTCTACTAG
ArgCysArgHis	ProProPro	GlySerHis	LeuLeuTyrAla	LysMetIle>
1260	1270	1280	1290	1300
* * *	* * *	* * *	* * *	* * *
CAGAAGCTAG	CCGACCTGCG	CAGCCTCAAT	GAGGAGCACT	CCAAGCAGTA
GTCTTCGATC	GGCTGGACGC	GTCCGAGTTA	CTCCTCGTGA	GGTTCGTTCAT
GlnLysLeu	AlaAspLeuArg	SerLeuAsn	GluGluHis	SerLysGlnTyr>

Title: "ISOFORMS OF THE HUMAN VITAMIN D
RECEPTOR"

Inventor: LINDA ANNE CROFTS, ET AL.

Application No.: 09/509,482

Atty. Docket No.: RICE-014

REPLACEMENT SHEET



FIG. 6D

```
          1310          1320          1330          1340          1350
      *      *      *      *      *      *      *      *      *
CCGCTGCCTC TCCTTCCAGC CTGAGTGCAG CATGAAGCTA ACGCCCCCTG
GGCGACGGAG AGGAAGGTCG GACTCACGTC GTACTTCGAT TGC GGGAAC
ArgCysLeu SerPheGln ProGluCysSer MetLysLeu ThrProLeu>

          1360          1370          1380
      *      *      *      *      *      *
TGCTCGAAGT GTTTGGCAAT GAGATCTCCT GA (SEQ ID NO:3)
ACGAGCTTCA CAAACCGTTA CTCTAGAGGA CT (SEQ ID NO:18)
ValLeuGluVal PheGlyAsn GluIleSer ***> (SEQ ID NO:10)
```

REPLACEMENT SHEET

FIG. 7A



Transcript 10

(Sequence Range: 1 to 1534)

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      10      20      30      40      50
      *      *      *      *      *
GTTTCCTTCT TCTGTCCGGG CGCCTTGGCA TGGAGTGGAG GAATAAGAAA
CAAAGGAAGA AGACAGCCCC GCGGAACCGT ACCTCACCTC CTTATTCTTT
MetGluTrpArg AsnLysLys>

      60      70      80      90     100
      *      *      *      *      *
AGGAGCGATT GGCTGTCGAT GGTGCTCAGA ACTGCTGGAG TGGAGGGGAT
TCCTCGCTAA CCGACAGCTA CCACGAGTCT TGACGACCTC ACCTCCCCTA
ArgSerAsp TrpLeuSerMet ValLeuArg ThrAlaGly ValGluGlyMet>

     110     120     130     140     150
      *      *      *      *      *
GGAGGCAATG GCGGCCAGCA CTTCCCTGCC TGACCCTGGA GACTTTGACC
CCTCCGTTAC CGCCGGTCGT GAAGGGACGG ACTGGGACCT CTGAAACTGG
GluAlaMet AlaAlaSer ThrSerLeuPro AspProGly AspPheAsp>

     160     170     180     190     200
      *      *      *      *      *
GGAACGTGCC CCGGATCTGT GGGGTGTGTG GAGACCGAGC CACTGGCTTT
CCTTGACAGG GGCCTAGACA CCCACACAC CTCTGGCTCG GTGACCGAAA
ArgAsnValPro ArgIleCys GlyValCys GlyAspArgAla ThrGlyPhe>

     210     220     230     240     250
      *      *      *      *      *
CACTTCAATG CTATGACCTG TGAAGGCTGC AAAGGCTTCT TCAGGTGAGC
GTGAAGTTAC GATACTGGAC ACTTCCGACG TTTCCGAAGA AGTCCACTCG
HisPheAsn AlaMetThrCys GluGlyCys LysGlyPhe PheArg*** (SEQ ID NO:11)

     260     270     280     290     300
      *      *      *      *      *
CCCCCTCCCA GGCTCTCCCC AGTGGAAAGG GAGGGAGAAG AAGCAAGGTG
GGGGGAGGGT CCGAGAGGGG TCACCTTTCC CTCCCTCTTC TTCGTTCCAC

     310     320     330     340     350
      *      *      *      *      *
TTTCCATGAA GGGAGCCCTT GCATTTTTC CACTCTCTTC CTTACAATGT
AAAGGTACTT CCCTCGGGAA CGTAAAAAGT GTAGAGGAAG GAATGTTACA

     360     370     380     390     400
      *      *      *      *      *
CCATGGAACA TGCGGCGCTC ACAGCCACAG GAGCAGGAGG GTCTTGCGCA
GGTACCTTGT ACGCCGCGAG TGTCGGTGTG CTCGTCCTCC CAGAACCGCT
```

REPLACEMENT SHEET



FIG. 7B

410	420	430	440	450
* *	* *	* *	* *	* *
AGCATGAAGC	GGAAGGCACT	ATTACCTGC	CCCTTCAACG	GGGACTGCCG
TCGTACTTCG	CCTTCCGTGA	TAAGTGGACG	GGAAGTTGC	CCCTGACGGC
460	470	480	490	500
* *	* *	* *	* *	* *
CATCACCAG	GACAACCGAC	GCCACTGCCA	GGCCTGCCGG	CTCAAACGCT
GTAAGTGGTTC	CTGTTGGCTG	CGGTGACGGT	CCGGACGGCC	GAGTTTGCGA
510	520	530	540	550
* *	* *	* *	* *	* *
GTGTGGACAT	CGGCATGATG	AAGGAGTTCA	TTCTGACAGA	TGAGGAAGTG
CACACCTGTA	GCCGTACTAC	TTCTCTCAAGT	AAGACTGTCT	ACTCCTTCAC
560	570	580	590	600
* *	* *	* *	* *	* *
CAGAGGAAGC	GGGAGATGAT	CCTGAAGCGG	AAGGAGGAGG	AGGCCTTGAA
GTCTCCTTCG	CCCTCTACTA	GGACTTCGCC	TTCTCTCTCC	TCCGGAACCTT
610	620	630	640	650
* *	* *	* *	* *	* *
GGACAGTCTG	CGGCCCAAGC	TGTCTGAGGA	GCAGCAGCGC	ATCATTGCCA
CCTGTCAGAC	GCCGGGTTCG	ACAGACTCCT	CGTCGTCGCG	TAGTAACGGT
660	670	680	690	700
* *	* *	* *	* *	* *
TACTGCTGGA	CGCCCACCAT	AAGACCTACG	ACCCACCTA	CTCCGACTTC
ATGACGACCT	GCGGGTGGTA	TTCTGGATGC	TGGGGTGGAT	GAGGCTGAAG
710	720	730	740	750
* *	* *	* *	* *	* *
TGCCAGTTCC	GGCCTCCAGT	TCGTGTGAAT	GATGGTGGAG	GGAGCCATCC
ACGGTCAAGG	CCGGAGGTCA	AGCACACTTA	CTACCACCTC	CCTCGGTAGG
760	770	780	790	800
* *	* *	* *	* *	* *
TTCCAGGCCC	AAGTCCAGAC	ACACTCCCAG	CTTCTCTGGG	GAAGAGACCC
AAGGTCCGGG	TTGAGGTCTG	TGTGAGGGTC	GAAGAGACCC	CTGAGGAGGA
810	820	830	840	850
* *	* *	* *	* *	* *
CCTCCTGCTC	AGATCACTGT	ATCACCTCTT	CAGACATGAT	GGACTCGTCC
GGAGGACGAG	TCTAGTGACA	TAGTGGAGAA	GTCTGTACTA	CCTGAGCAGG
860	870	880	890	900
* *	* *	* *	* *	* *
AGCTTCTCCA	ATCTGGATCT	GAGTGAAGAA	GATTCAGATG	ACCCTTCTGT
TCGAAGAGGT	TAGACCTAGA	CTCACTTCTT	CTAAGTCTAC	TGGGAAGACA
910	920	930	940	950
* *	* *	* *	* *	* *
GACCCTAGAG	CTGTCCCAGC	TCTCCATGCT	GCCCCACCTG	GCTGACCTGG
CTGGGATCTC	GACAGGGTCG	AGAGGTACGA	CGGGGTGGAC	CGACTGGACC

REPLACEMENT SHEET



FIG. 7C

960	970	980	990	1000
* *	* *	* *	* *	* *
TCAGTTACAG	CATCCAAAAG	GTCATTGGCT	TTGCTAAGAT	GATACCAGGA
AGTCAATGTC	GTAGGTTTTC	CAGTAACCGA	AACGATTCTA	CTATGGTCTT
1010	1020	1030	1040	1050
* *	* *	* *	* *	* *
TTCAGAGACC	TCACCTCTGA	GGACCAGATC	GTACTGCTGA	AGTCAAGTGC
AAGTCTCTGG	AGTGGAGACT	CCTGGTCTAG	CATGACGACT	TCAGTTCACG
1060	1070	1080	1090	1100
* *	* *	* *	* *	* *
CATTGAGGTC	ATCATGTTGC	GCTCCAATGA	GTCCTTCACC	ATGGACGACA
GTAACCTCCAG	TAGTACAACG	CGAGGTACT	CAGGAAGTGG	TACCTGCTGT
1110	1120	1130	1140	1150
* *	* *	* *	* *	* *
TGTCCTGGAC	CTGTGGCAAC	CAAGACTACA	AGTACCGCGT	CAGTGACGTG
ACAGGACCTG	GACACCGTTG	GTTCTGATGT	TCATGGCGCA	GTCACTGCAC
1160	1170	1180	1190	1200
* *	* *	* *	* *	* *
ACCAAAGCCG	GACACAGCCT	GGAGCTGATT	GAGCCCCTCA	TCAAGTTCCA
TGGTTTCGGC	CTGTGTCGGA	CCTCGACTAA	CTCGGGGAGT	AGTTCAAGGT
1210	1220	1230	1240	1250
* *	* *	* *	* *	* *
GGTGGGACTG	AAGAAGCTGA	ACTTGCATGA	GGAGGAGCAT	GTCTGTCTCA
CCACCCTGAC	TTCTTCGACT	TGAACGTACT	CCTCCTCGTA	CAGGACGAGT
1260	1270	1280	1290	1300
* *	* *	* *	* *	* *
TGGCCATCTG	CATCGTCTCC	CCAGATCGTC	CTGGGGTGCA	GGACGCCGCG
ACCGGTAGAC	GTAGCAGAGG	GGTCTAGCAG	GACCCACGT	CCTGCGGCGC
1310	1320	1330	1340	1350
* *	* *	* *	* *	* *
CTGATTGAGG	CCATCCAGGA	CCGCCTGTCC	AACACACTGC	AGACGTACAT
GACTAACTCC	GGTAGGTCCT	GGCGGACAGG	TTGTGTGACG	TCTGCATGTA
1360	1370	1380	1390	1400
* *	* *	* *	* *	* *
CCGCTGCCGC	CACCCGCCCC	CGGGCAGCCA	CCTGCTCTAT	GCCAAGATGA
GGCGACGGCG	GTGGGCGGGG	GCCCGTCGGT	GGACGAGATA	CGGTTCTACT
1410	1420	1430	1440	1450
* *	* *	* *	* *	* *
TCCAGAAGCT	AGCCGACCTG	CGCAGCCTCA	ATGAGGAGCA	CTCCAAGCAG
AGGTCTTCGA	TGGGCTGGAC	GCGTCGGAGT	TACTCCTCGT	GAGGTTCGTC
1460	1470	1480	1490	1500
* *	* *	* *	* *	* *
TACCGCTGCC	TCTCCTTCCA	GCCTGAGTGC	AGCATGAAGC	TAACGCCCCCT
ATGGCGACGG	AGAGGAAGGT	CGGACTCAGC	TCGTACTTCG	ATTGCGGGGA

Title: "ISOFORMS OF THE HUMAN VITAMIN D
RECEPTOR"

Inventor: LINDA ANNE CROFTS, ET AL.

Application No.: 09/509,482

Atty. Docket No.: RICE-014

REPLACEMENT SHEET



FIG. 7D

	1510		1520		1530
*	*	*	*	*	*
TGTGCTCGAA	GTGTTTGGCA	ATGAGATCTC	CTGA	(SEQ ID NO:4)	
ACACGAGCTT	CACAAACCGT	TACTCTAGAG	GACT	(SEQ ID NO:19)	

REPLACEMENT SHEET



FIG. 8A

10	20	30	40	50
*	*	*	*	*
TGCGACCTTG	GCGGTGAGCC	TGGGGACAGG	GGTGAGGCCA	GAGACGGACG
ACGCTGGAAC	CGCCTCGG	ACCCCTGTCC	CCACTCCGGT	CTCTGCCTGC
60	70	80	90	100
*	*	*	*	*
GACGCAGGGG	CCCGGCCCAA	GGCGAGGGAG	AACAGCGGCA	CTAAGGCAGA
CTGCGTCCCC	GGGCCGGGTT	CCGCTCCCTC	TTGTCGCCGT	GATTCCGTCT
110	120	130	140	150
*	*	*	*	*
AAGGAAGAGG	GCGGTGTGTT	CACCCGCAGC	CCAATCCATC	ACTCAGCAAC
TTCCTTCTCC	CGCCACACAA	GTGGGCGTCG	GGTTAGGTAG	TGAGTCGTTG
160	170	180	190	200
*	*	*	*	*
TCCTAGACGC	TGGTAGAAAG	TTCCTCCGAG	GAGCCTGCCA	TCCAGTCGTG
AGGATCTGCG	ACCATCTTTC	AAGGAGGCTC	CTCGGACGGT	AGGTCAGCAC
210	220	230	240	250
*	*	*	*	*
CGTGCAGAAG	CCTTTGGGTC	TGAAGTGTCT	GTGAGACCTC	ACAGAAGAGC
GCACGTCTTC	GGAAACCCAG	ACTTCACAGA	CACTCTGGAG	TGTCTTCTCG
260	270	280	290	300
*	*	*	*	*
ACCCCTGGGC	TCCACTTACC	TGCCCCCTGC	TCCTTCAGGG	ATGGAGGCAA
TGGGGACCCG	AGGTGAATGG	ACGGGGGACG	AGGAAGTCCC	TACCTCCGTT
				MetGluAla>
310	320	330	340	350
*	*	*	*	*
TGGCGGCCAG	CACTTCCCTG	CCTGACCCTG	GAGACTTTGA	CCGGAACGTG
ACCGCCGGTC	GTGAAGGGAC	GGACTGGGAC	CTCTGAAACT	GGCCTTGCAC
MetAlaAlaSer	ThrSerLeu	ProAspPro	GlyAspPheAsp	ArgAsnVal>
360	370	380	390	400
*	*	*	*	*
CCCCGGATCT	GTGGGGTGTG	TGGAGACCGA	GCCACTGGCT	TTCACTTCAA
GGGGCCTAGA	CACCCACAC	ACCTCTGGCT	CGGTGACCGA	AAGTGAAGTT
ProArgIle	CysGlyValCys	GlyAspArg	AlaThrGly	PheHisPheAsn>
410	420	430	440	450
*	*	*	*	*
TGCTATGACC	TGTGAAGGCT	GCAAAGGCTT	CTTCAGGCGA	AGCATGAAGC
ACGATACTGG	AACTTCCGA	CGTTTCCGAA	GAAGTCCGCT	TCGTACTTCG
AlaMetThr	CysGluGly	CysLysGlyPhe	PheArgArg	SerMetLys>
460	470	480	490	500
*	*	*	*	*
GGAAGGCACT	ATTACCTGC	CCCTTCAACG	GGGACTGCCG	CATCACCAAG
CCTTCCGTGA	TAAGTGGACG	GGGAAGTTGC	CCCTGACGGC	GTAGTGGTTC
ArgLysAlaLeu	PheThrCys	ProPheAsn	GlyAspCysArg	IleThrLys>

REPLACEMENT SHEET



FIG. 8B

510 520 530 540 550
* * * * *
GACAACCGAC GCCACTGCCA GGCCTGCCGG CTCAAACGCT GTGTGGACAT
CTGTTGGCTG CCGTGACGGT CCGGACGGCC GAGTTTGCGA CACACCTGTA
AspAsnArg ArgHisCysGln AlaCysArg LeuLysArg CysValAspIle>

560 570 580 590 600
* * * * *
CGGCATGATG AAGGAGTTCA TTCTGACAGA TGAGGAAGTG CAGAGGAAGC
GCCGTACTAC TTCCTCAAGT AAGACTGTCT ACTCCTTCAC GTCTCCTTCG
GlyMetMet LysGluPhe IleLeuThrAsp GluGluVal GlnArgLys>

610 620 630 640 650
* * * * *
GGGAGATGAT CCTGAAGCGG AAGGAGGAGG AGGCCTTGAA GGACAGTCTG
CCCTCTACTA GGACTTCGCC TTCCTCCTCC TCCGGAACCTT CCTGTCTAGAC
ArgGluMetIle LeuLysArg LysGluGlu GluAlaLeuLys AspSerLeu>

660 670 680 690 700
* * * * *
CGGCCCAAGC TGTCTGAGGA GCAGCAGCGC ATCATTGCCA TACTGCTGGA
GCCGGGTTCG ACAGACTCCT CGTCGTCGCG TAGTAACGGT ATGACGACCT
ArgProLys LeuSerGluGlu GlnGlnArg IleIleAla IleLeuLeuAsp>

710 720 730 740 750
* * * * *
CGCCCACCAT AAGACCTACG ACCCCACCTA CTCCGACTTC TGCCAGTTCC
GCGGGTGGTA TTCTGGATGC TGGGGTGGAT GAGGCTGAAG ACGGTCAAGG
AlaHisHis LysThrTyr AspProThrTyr SerAspPhe CysGlnPhe>

760 770 780 790 800
* * * * *
GGCCTCCAGT TCGTGTGAAT GATGGTGGAG GGAGCCATCC TTCCAGGCCC
CCGGAGGTCA AGCACACTTA CTACCACCTC CCTCGGTAGG AAGGTCCGGG
ArgProProVal ArgValAsn AspGlyGly GlySerHisPro SerArgPro>

810 820 830 840 850
* * * * *
AACTCCAGAC ACACTCCAG CTTCTCTGGG GACTCCTCCT CCTCCTGCTC
TTGAGGTCTG TGTGAGGGTC GAAGAGACCC CTGAGGAGGA GGAGGACGAG
AsnSerArg HisThrProSer PheSerGly AspSerSer SerSerCysSer>

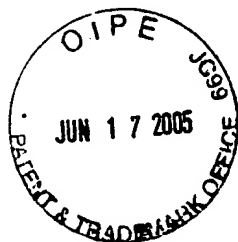
860 870 880 890 900
* * * * *
AGATCACTGT ATCACCTCTT CAGACATGAT GGA CTCTCTCCA
TCTAGTGACA TAGTGGAGAA GTCTGTACTA CCTGAGCAGG TCGAAGAGGT
AspHisCys IleThrSer SerAspMetMet AspSerSer SerPheSer>

910 920 930 940 950
* * * * *
ATCTGGATCT GAGTGAAGAA GATTCAGATG ACCCTTCTGT GACCCTAGAG
TAGACCTAGA CTCACCTCTT CTAAGTCTAC TGGGAAGACA CTGGGATCTC
AsnLeuAspLeu SerGluGlu AspSerAsp AspProSerVal ThrLeuGlu>

960 970 980 990 1000
* * * * *
CTGTCCAGC TCTCCATGCT GCCCCACCTG GCTGACCTGG TCAGTTACAG
GACAGGGTCG AGAGGTACGA CGGGGTGGAC CGACTGGACC AGTCAATGTC
LeuSerGln LeuSerMetLeu ProHisLeu AlaAspLeu ValSerTyrSer>

REPLACEMENT SHEET

FIG. 8C



1010 *	1020 *	1030 *	1040 *	1050 *
CATCCAAAAG	GTCATTGGCT	TTGCTAAGAT	GATACCAGGA	TTCAGAGACC
GTAGGTTTTT	CAGTAACCGA	AACGATTCTA	CTATGGTCCT	AAGTCTCTGG
IleGlnLys	ValIleGly	PheAlaLysMet	IleProGly	PhēArgAsp>
1060 *	1070 *	1080 *	1090 *	1100 *
TCACCTCTGA	GGACCAGATC	GTA CTGCTGA	AGTCAAGTGC	CATTGAGGTC
AGTGGAGACT	CCTGGTCTAG	CATGACGACT	TCAGTTCACG	GTA ACTCCAG
LeuThrSerGlu	AspGlnIle	ValLeuLeu	LysSerSerAla	IleGluVal>
1110 *	1120 *	1130 *	1140 *	1150 *
ATCATGTTGC	GCTCCAATGA	GTCCTTCACC	ATGGACGACA	TGTCCTGGAC
TAGTACAACG	CGAGGTTACT	CAGGAAGTGG	TACCTGCTGT	ACAGGACCTG
IleMetLeu	ArgSerAsnGlu	SerPheThr	MetAspAsp	MetSerTrpThr>
1160 *	1170 *	1180 *	1190 *	1200 *
CTGTGGCAAC	CAAGACTACA	AGTACCGCGT	CAGTGACGTG	ACCAAAGCCG
GACACCGTTG	GTTCTGATGT	TCATGGCGCA	GTC ACTGCAC	TGGTTTCGGC
CysGlyAsn	GlnAspTyr	LysTyrArgVal	SerAspVal	ThrLysAla>
1210 *	1220 *	1230 *	1240 *	1250 *
GACACAGCCT	GGAGCTGATT	GAGCCCCTCA	TCAAGTTCCA	GGTGGGACTG
CTGTGTCTGA	CCTCGACTAA	CTCGGGGAGT	AGTTCAAGGT	CCACCCTGAC
GlyHisSerLeu	GluLeuIle	GluProLeu	IleLysPheGln	ValGlyLeu>
1260 *	1270 *	1280 *	1290 *	1300 *
AAGAAGCTGA	ACTTG CATGA	GGAGGAGCAT	GTCCTGCTCA	TGGCCATCTG
TTCTTCGACT	TGAACGTACT	CCTCCTCGTA	CAGGACGAGT	ACCGGTAGAC
LysLysLeu	AsnLeuHisGlu	GluGluHis	ValLeuLeu	MetAlaIleCys>
1310 *	1320 *	1330 *	1340 *	1350 *
CATCGTCTCC	CCAGATCGTC	CTGGGGTGCA	GGACGCCGCG	CTGATTGAGG
GTAGCAGAGG	GGTCTAGCAG	GACCCACAGT	CCTGCGGCGC	GACTAACTCC
IleValSer	ProAspArg	ProGlyValGln	AspAlaAla	LeuIleGlu>
1360 *	1370 *	1380 *	1390 *	1400 *
CCATCCAGGA	CCGCCTGTCC	AACACACTGC	AGACGTACAT	CCGCTGCCGC
GGTAGGTCCT	GGCGGACAGG	TTGTGTGACG	TCTGCATGTA	GGCGACGGCG
AlaIleGlnAsp	ArgLeuSer	AsnThrLeu	GlnThrTyrIle	ArgCysArg>
1410 *	1420 *	1430 *	1440 *	1450 *
CACCCGCCCC	CGGGCAGCCA	CCTGCTCTAT	GCCAAGATGA	TCCAGAAGCT
GTGGGCGGGG	GCCCGTCGGT	GGACGAGATA	CGGTTCTACT	AGGTCTTCGA
HisProPro	ProGlySerHis	LeuLeuTyr	AlaLysMet	IleGlnLysLeu>
1460 *	1470 *	1480 *	1490 *	1500 *
AGCCGACCTG	CGCAGCCTCA	ATGAGGAGCA	CTCCAAGCAG	TACCGCTGCC
TCGGCTGGAC	GCGTCGGAGT	TACTCCTCGT	GAGGTTCTGC	ATGGCGACGG
AlaAspLeu	ArgSerLeu	AsnGluGluHis	SerLysGln	TyrArgCys>

Title: "ISOFORMS OF THE HUMAN VITAMIN D
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Inventor: LINDA ANNE CROFTS, ET AL.
Application No.: 09/509,482
Atty. Docket No.: RICE-014

REPLACEMENT SHEET

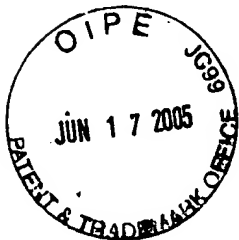


FIG. 8D

1510	1520	1530	1540	1550
*	*	*	*	*
TCTCCTTCCA	GCCTGAGTGC	AGCATGAAGC	TAACGCCCCT	TGTGCTCGAA
AGAGGAAGGT	CGGACTCACG	TCGTACTTCG	ATTGCGGGGA	ACACGAGCTT
LeuSerPheGln	ProGluCys	SerMetLys	LeuThrProLeu	ValLeuGlu>
1560	1570			
*	*			
GTGTTTGGCA	ATGAGATCTC	CTGA	(SEQ ID NO:7)	
CACAAACCGT	TACTCTAGAG	GA	(SEQ ID NO:20)	
ValPheGly	AsnGluIleSer	***>	(SEQ ID NO:12)	